WHAT IS CLAIMED IS:

CallSeq™

Sub B1

1. In a computer system, a method of identifying an unknown base in a sample nucleic acid sequence, said method comprising the steps of:

inputting a plurality of probe intensities, each of said probe intensities being associated with a probe on a chip;

said computer system comparing said plurality of probe intensities wherein each of said plurality of probe intensities is substantially proportional to a probe hybridizing with at least one sequence; and

calling said unknown base according to said comparison of said plurality of probe intensities.

2. The method of claim 1, wherein said at least one sequence includes said sample sequence.

Sub B2

3. The method of claim 2, further comprising the step of said computer system calculating a ratio of a higher probe intensity to a lower probe intensity.

4. The method of claim 3, further comprising the step of calling said unknown base as being a base complement of said probe associated with said higher probe intensity if said ratio is greater than a predetermined ratio value.

5. The method of claim 3, wherein said ratio is approximately 1.2.

Sub B3

6. The method of claim 2, further comprising the step of sorting said plurality of probe intensities.

7. The method of claim 1, wherein said at least one sequence includes said sample sequence and a reference sequence.

8. The method of claim 7, further comprising the step of said computer system comparing probe intensities of a probe hybridizing with said sample sequence to probe intensities hybridizing with said reference sequence.

9. The method of claim 7, further comprising the step of calculating first ratios of a wild-type probe intensity to each probe intensity of a probe hybridizing with said reference sequence, wherein said wild-type probe intensity is associated with a wild-type probe.

10. The method of claim 9, further comprising the step of calculating second ratios of the highest probe intensity of a probe hybridizing with said sample sequence to each probe intensity of a probe hybridizing with said sample sequence.

11. The method of claim 10, further comprising the step of calculating third ratios of said first ratios to said second ratios.

12. The method of claim 7, further comprising the step of comparing neighboring probe intensities of said plurality of probe intensities.

13. The method of claim 7, wherein probe intensities of a probe hybridizing with said reference sequence are from a plurality of experiments.

14. The method of claim 13, further comprising the step of said computer system comparing probe intensities of a probe hybridizing with said sample sequence to statistics about said plurality of experiments.

15. The method of claim 14, wherein said statistics include a mean and standard deviation.

16. The method of claim 13, further comprising the step of normalizing said plurality of probe intensities by dividing each probe intensity by a sum of related probe intensities.

17. The method of claim 1, further comprising the step of subtracting a background intensity from each of said plurality of probe intensities.

18. The method of claim 1, further comprising the step of setting a probe intensity equal to a relative small positive number if said probe intensity is less than or equal to zero.

19. The method of claim 1, further comprising the step of indicating said unknown base is unable to be called if said plurality of probe intensities have insufficient intensity to call said unknown base.

20. The method of claim 1, wherein said unknown base is called as being A, C, G, or T.

Pooling Processing

21. A method of processing first and second nucleic acid sequences, comprising the steps of:

providing a plurality of nucleic acid probes;

labeling said first nucleic acid sequence with a first marker;

labeling said second nucleic acid sequence with a second marker; and

hybridizing said first and second labeled nucleic acid sequences at the same time.

22. The method of claim 21, wherein said plurality of nucleic acid probes are on a chip.

23. The method of claim 21, further comprising the step of fragmenting said first and second nucleic acid sequences at the same time.

24. The method of claim 21, further comprising the step of scanning for said first and second markers on said chip, said first and second labeled nucleic acid sequences being on said chip.

25. The method of claim 21, wherein said first and second markers are fluorescent markers.

26. The method of claim 25, wherein said first and second markers emit light at different wavelengths upon excitation.

ViewSeq™

27. In a computer system, a method of analyzing a plurality of sequences of bases, said plurality of sequences including at least one reference sequence and at least one sample sequence, the method comprising the steps of:

displaying said at least one reference sequence in a first area on a display device; and

displaying said at least one sample sequence in a second area on said display device;

whereby a user is capable of visually comparing said plurality of sequences.

28. The method of claim 27, wherein said plurality of sequences are monomer strands of DNA or RNA.

29. The method of claim 27, wherein said bases are A, C, G, or T.

30. The method of claim 27, wherein said at least one reference sequence includes a chip wild-type that has been tiled on a chip.

31. The method of claim 30, wherein said chip wild-type sequence is displayed as a first sequence in said first area.

32. The method of claim 30, further comprising the step of displaying a label in said first area to identify said chip wild-type sequence.

33. The method of claim 32, wherein said label is a capital C.

34. The method of claim 27, wherein said at least one sample sequence has been hybridized on a chip.

35. The method of claim 27, further comprising the step of indicating bases that differ among a plurality of user selected sequences.

36. The method of claim 27, further comprising the steps of:

displaying a name associated with each of said at least one reference sequence in said first area; and

displaying a name associated with each of said at least one sample sequence in said second area.

37. The method of claim 27, further comprising the step of linking at least one reference sequence in said first area with at least one sample sequence in said second area.

38. The method of claim 37, further comprising the step of indicating on said display device which sequences are linked.

39. The method of claim 38, wherein said indicating step includes the step of displaying a common symbol next to said linked sequences.

40. The method of claim 39, wherein said common symbol is a link number.

41. The method of claim 37, further comprising the step of indicating bases of said at least one sample sequence that are not equal to a corresponding base in said at least one reference sequence.

42. The method of claim 27, wherein said at least one reference sequence and said at least one sample sequence are aligned on said display device.

43. The method of claim 27, further comprising the step of exposing sequences to probes.

44. The method of claim 43, further comprising the step of evaluating said exposed sequences according to hybridization with said probes.

add B7

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